Exhibit II

⚗ NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 50   expect: 10.000 wordsize: 11   Filter ☑ View option Standard   ▾
Masking character option X for protein, n for nucleotide ▾   Masking color option Black ▾
☐ Show CDS translation   Align

Sequence 1: gi|4454551|gb|AF113003.1|AF113003 SEQ ID NO:4
Length = 3094 (1 .. 3094)

Sequence 2: gi|4559297|gb|AF125672.1|AF125672
Length = 8686 (1 .. 8686)
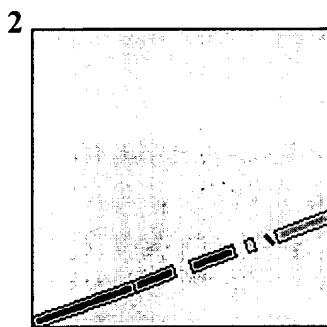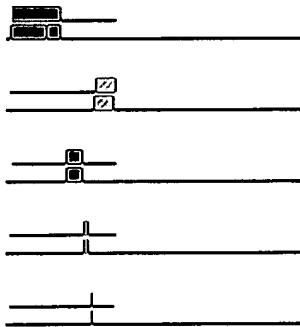
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.


```
Score = 2680 bits (1394),  Expect = 0.0
Identities = 1465/1480 (98%), Gaps = 3/1480 (0%)
Strand=Plus/Plus

Query  1    CATGTCGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC  60
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  156  CATGTCGGGCTCCACACAGCCTGTGGCACAGACGTGGAGGGCCACTGAGCCCCGCTACCC  215

Query  61   GCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGACGCACACGGACGTCGGGCTCCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216  GCCCCACAGCCTTTCCTACCCAGTGCAGATCGCCCGGACGCACACGGACGTCGGGCTCCT  275

Query  121  GGAGTACCAGCACCACTCCCGCGACTATGCCTCCCACCTGTCGCCGGGCTCCATCATCCA  180
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                       |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct   276   GGAGTACCAGCACCACTCCCGCGACTATGCCTCCCACCTGTCGCCCGGCTCCATCATCCA   335

Query   181   GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCCGGGAATGAACGGTCCCA   240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   336   GCCCCAGCGGCGGAGGCCCTCCCTGCTGTCTGAGTTCCAGCCCGGGAATGAACGGTCCCA   395

Query   241   GGAGCTCCACCTGCGGCCAGAGTCCCACTCATACCTGCCCGAGCTGGGGAAGTCAGAGAT   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   396   GGAGCTCCACCTGCGGCCAGAGTCCCACTCATACCTGCCCGAGCTGGGGAAGTCAGAGAT   455

Query   301   GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCCTGCTGCGACC   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   456   GGAGTTCATTGAAAGCAAGCGCCCTCGGCTAGAGCTGCTGCCTGACCCCCTGCTGCGACC   515

Query   361   GTCACCCCTGCTGGCCACGGGCCAGCCTGCGGGATCTGAAGACCTCACCAAGGACCGTAG   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   516   GTCACCCCTGCTGGCCACGGGCCAGCCTGCGGGATCTGAAGACCTCACCAAGGACCGTAG   575

Query   421   CCTGACGGGCAAGCTGGAACCGGTGTCTnnnnnnnnnnnnnnnGCACACTGACCCTGAGCT   480
              ||||||||||||||||||||||||||||           ||||||||||||||||||||||
Sbjct   576   CCTGACGGGCAAGCTGGAACCGGTGTCTCCCCCCAGCCCCCCGCACACTGACCCTGAGCT   635

Query   481   GGAGCTGGTGCCGCCACGGCTGTCCAAGGAGGAGCTGATCCAGAACATGGACCGCGTGGA   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   636   GGAGCTGGTGCCGCCACGGCTGTCCAAGGAGGAGCTGATCCAGAACATGGACCGCGTGGA   695

Query   541   CCGAGAGATCACCATGGTAGAGCAGCAGATCTCTAAGCTGAAGAAGAAGCAGCAACAGCT   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   696   CCGAGAGATCACCATGGTAGAGCAGCAGATCTCTAAGCTGAAGAAGAAGCAGCAACAGCT   755

Query   601   GGAGGAGGAGGCTGCCAAGCCGCCCGAGCCTGAGAAGCCCGTGTCACCGCCGCCCATCGA   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   756   GGAGGAGGAGGCTGCCAAGCCGCCCGAGCCTGAGAAGCCCGTGTCACCGCCGCCCATCGA   815

Query   661   GTCGAAGCACCGCAGCCTGGTGCAGATCATCTACGACGAGAACCGGAAGAAGGCTGAAGC   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   816   GTCGAAGCACCGCAGCCTGGTGCAGATCATCTACGACGAGAACCGGAAGAAGGCTGAAGC   875

Query   721   TGCACATCGGATTCTGGAAGGCCTGGGGCCCCAGGTGGAGCTGCCGCTGTACAACCAGCC   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   876   TGCACATCGGATTCTGGAAGGCCTGGGGCCCCAGGTGGAGCTGCCGCTGTACAACCAGCC   935

Query   781   CTCCGACACCCGGCAGTATCATGAGAACATCAAAATAAACCAGGCGATGCGGAAGAAGCT   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   936   CTCCGACACCCGGCAGTATCATGAGAACATCAAAATAAACCAGGCGATGCGGAAGAAGCT   995

Query   841   AATCTTGTACTTCAAGAGGAGGAATCACGCTCGGAAACAATGGAAGCAGAAGTTCTGCCA   900
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct   996   AATCTTGTACTTCAAGAGGAGGAATCACGCTCGGAAACAATGGGAGCAGAAGTTCTGCCA   1055

Query   901   GCGCTATGACCAGCTCATGGAGGCCTTGGnnnnnnnGGTGGAGCGCATCGAAAACAACCC   960
              |||||||||||||||||||||||||| ||| || ||||||||||||||| ||||||||
Sbjct   1056  GCGCTATGACCAGCTCATGGAGGCCTGGGAGAAGAAGGTGGAGCGCATCGAGAACAACCC   1115

Query   961   GCGCCGGCGGGCCAAGGAGAGCAAGGTGCGCGAGTACTACGAAAAGCAGTTCCCTGAGAT   1020
              || ||||||||||||||||||||||||| ||||||||||||| |||||||||||||||||
Sbjct   1116  CCGGCGGCGGGCCAAGGAGAGCAAGGTTCGCGAGTACTACGAGAAGCAGTTCCCTGAGAT   1175

Query   1021  CCGCAAGCAGCGCGAGCTGCAGGAGCGCATGCAGAGCAGGGTGGGCCAGCGGGGCAGTGG   1080
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                 ||||||||||||||||||||||||||||||||||||||      |||||||||||||||||||||||||||||
Sbjct   1176     CCGCAAGCAGCGCGAGCTGCAGGAGCGCATGCAG---AGGGTGGGCCAGCGGGGCAGTGG     1232

Query   1081     GCTGTCCATGTCGGCCGCCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC     1140
                 |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1233     GCTGTCCATGTCGCCCGCCCGCAGCGAGCACGAGGTGTCAGAGATCATCGATGGCCTCTC     1292

Query   1141     AGAGCAGGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCCGTGATCCCGCCCATGCTGTA     1200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1293     AGAGCAGGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCCGTGATCCCGCCCATGCTGTA     1352

Query   1201     CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGGCTTATGGCCGACCCCAT     1260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1353     CGACGCTGACCAGCAGCGCATCAAGTTCATCAACATGAACGGGCTTATGGCCGACCCCAT     1412

Query   1261     GAAGGTGTACAAAGACCGCCAGGTCATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT     1320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1413     GAAGGTGTACAAAGACCGCCAGGTCATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTT     1472

Query   1321     CCGGGAGAAGTTCATGCAGCATCCCAAGAACTTTGGCCTGATCGCATCATTCCTGGAGAG     1380
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1473     CCGGGAGAAGTTCATGCAGCATCCCAAGAACTTTGGCCTGATCGCATCATTCCTGGAGAG     1532

Query   1381     GAAGACAGTGGCTGAGTGCGTCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA     1440
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1533     GAAGACAGTGGCTGAGTGCGTCCTCTATTACTACCTGACTAAGAAGAATGAGAACTATAA     1592

Query   1441     GAGCCTGGTGAGACGGAGCTATCGGCGCCGCGGCAAGAGC       1480
                 ||||||||||||||||||||||||||||||||||||||||
Sbjct   1593     GAGCCTGGTGAGACGGAGCTATCGGCGCCGCGGCAAGAGC       1632
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Score = 1013 bits (527),   Expect = 0.0
Identities = 561/564 (99%), Gaps = 0/564 (0%)
Strand=Plus/Plus
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Query   2531     AAGCCCCCCGCGGCTGAGGAGCTGGCAGTGGACACAGGGAAGGCCGAGGAGCCCGTCAAG     2590
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2632     AAGCCCCCCGCGGCTGAGGAGCTGGCAGTGGACACAGGGAAGGCCGAGGAGCCCGTCAAG     2691

Query   2591     AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCGGCCAAGGGCAAGGACGCGGAGGCCGCT     2650
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2692     AGCGAGTGCACGGAGGAAGCCGAGGAGGGGCCGGCCAAGGGCAAGGACGCGGAGGCCGCT     2751

Query   2651     GAGGCCACGGCCGAGGGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGGCC     2710
                 |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Sbjct   2752     GAGGCCACGGCCGAGAGGGCGCTCAAGGCAGAGAAGAAGGAGGGCGGGAGCGGCAGGGCC     2811

Query   2711     ACCACTGCCAAGAGCTCGGGCGCCCCCCAGGACAGCGACTCCAGTGCTACCTGCAGTGCA     2770
                 |||||  |||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Sbjct   2812     ACCACAGCCAAGAGCTCGGGCGCCCCCCAGGACAGCGACTCCAGTGCCACCTGCAGTGCA     2871

Query   2771     GACGAGGTGGATGAGGCCGAGGGCGGCGACAAGAACCGGCTGCTGTCCCCAAGGCCCAGC     2830
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2872     GACGAGGTGGATGAGGCCGAGGGCGGCGACAAGAACCGGCTGCTGTCCCCAAGGCCCAGC     2931
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Query   2831   CTCCTCACCCCGACTGGCGACCCCCGGGCCAATGCCTCACCCCAGAAGCCACTGGACCTG   2890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2932   CTCCTCACCCCGACTGGCGACCCCCGGGCCAATGCCTCACCCCAGAAGCCACTGGACCTG   2991

Query   2891   AAGCAGCTGAAGCAGCGAGCGGCTGCCATnnnnnnnnATCCAGGTCACCAAAGTCCATGAG   2950
               ||||||||||||||||||||||||||||||                ||||||||||||||||||||||||||||||
Sbjct   2992   AAGCAGCTGAAGCAGCGAGCGGCTGCCATCCCCCCCATCCAGGTCACCAAAGTCCATGAG   3051

Query   2951   nnnnnnnGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCCAGCCCCACCGCCACCGCAA   3010
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3052   CCCCCCCGGGAGGACGCAGCTCCCACCAAGCCAGCTCCCCCAGCCCCACCGCCACCGCAA   3111

Query   3011   AACCTGCAGCCGGAGAGCGACGCCCCTCAGCAGCCTGGCAGCAGCCCCCGGGGCAAGAGC   3070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3112   AACCTGCAGCCGGAGAGCGACGCCCCTCAGCAGCCTGGCAGCAGCCCCCGGGGCAAGAGC   3171

Query   3071   AGGAGCCCGGCACCCCCCGCCGAC   3094
               ||||||||||||||||||||||||
Sbjct   3172   AGGAGCCCGGCACCCCCCGCCGAC   3195
```

Score = 898 bits (467), Expect = 0.0
Identities = 467/467 (100%), Gaps = 0/467 (0%)
Strand=Plus/Plus

```
Query   1633   CCTCCTCAAGGAGAAGACAGACGACACCTCAGGGGAGGACAACGACGAGAAGGAGGCTGT   1692
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1785   CCTCCTCAAGGAGAAGACAGACGACACCTCAGGGGAGGACAACGACGAGAAGGAGGCTGT   1844

Query   1693   GGCCTCCAAAGGCCGCAAAACTGCCAACAGCCAGGGAAGACGCAAAGGCCGCATCACCCG   1752
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1845   GGCCTCCAAAGGCCGCAAAACTGCCAACAGCCAGGGAAGACGCAAAGGCCGCATCACCCG   1904

Query   1753   CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCCAGCAGAGCGCCGAGCT   1812
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1905   CTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCCAGCAGAGCGCCGAGCT   1964

Query   1813   GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAAGAAGAAATGGAAACAGCCAA   1872
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1965   GGCCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAAGAAGAAATGGAAACAGCCAA   2024

Query   1873   GAAAGGTCTCCTGGAACACGGCCGCAACTGGTCGGCCATCGCCCGGATGGTGGGCTCCAA   1932
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2025   GAAAGGTCTCCTGGAACACGGCCGCAACTGGTCGGCCATCGCCCGGATGGTGGGCTCCAA   2084

Query   1933   GACTGTGTCGCAGTGTAAGAACTTCTACTTCAACTACAAGAAGAGGCAGAACCTCGATGA   1992
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2085   GACTGTGTCGCAGTGTAAGAACTTCTACTTCAACTACAAGAAGAGGCAGAACCTCGATGA   2144

Query   1993   GATCTTGCAGCAGCACAAGCTGAAGATGGAGAAGGAGAGGAACGCGCGGAGGAAGAAGAA   2052
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2145   GATCTTGCAGCAGCACAAGCTGAAGATGGAGAAGGAGAGGAACGCGCGGAGGAAGAAGAA   2204

Query   2053   GAAAGCGCCGGCGGCGGCCAGCGAGGAGGCTGCATTCCCGCCCGTGG   2099
```

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               ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2205   GAAAGCGCCGGCGGCGGCCAGCGAGGAGGCTGCATTCCCGCCCGTGG      2251
```

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    _____Ω_____
    _____Ω_____
```

```
Score =  154 bits (80),  Expect = 2e-33
Identities = 80/80 (100%), Gaps = 0/80 (0%)
Strand=Plus/Plus
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```
Query  2218   AGCCACTGTCAACAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC  2277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2319   AGCCACTGTCAACAACAGCTCAGACACCGAGAGCATCCCCTCTCCTCACACTGAGGCCGC  2378

Query  2278   CAAGGACACAGGGCAGAATG  2297
              ||||||||||||||||||||
Sbjct  2379   CAAGGACACAGGGCAGAATG  2398
```

```
    _____Ω_____
    _____Ω_____
```

```
Score = 48.8 bits (25),  Expect = 0.12
Identities = 27/28 (96%), Gaps = 0/28 (0%)
Strand=Plus/Plus
```

```
Query  2444   CCCTCTGCACCTCCTCCTGTGGTCCCCA  2471
              ||||||| ||||||||||||||||||||
Sbjct  2545   CCCTCTTCACCTCCTCCTGTGGTCCCCA  2572
```

```
CPU time:       0.05 user secs.        0.02 sys. secs        0.07 total secs.

Lambda      K        H
    1.33    0.621    1.12

Gapped
Lambda      K        H
    1.33    0.621    1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1177
Number of extensions: 44
Number of successful extensions: 7
Number of sequences better than 10.0: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 5
Length of query: 3094
Length of database: 17,886,619,220
Length adjustment: 27
Effective length of query: 3067
```

Effective length of database: 17,886,619,193
Effective search space: 54858261064931
Effective search space used: 54858261064931
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 16 (31.5 bits)
S2: 22 (43.0 bits)